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RAW SEQUENCE LISTING DATE: 09/19/2000
 PATENT APPLICATION: US/09/653,961 TIME: 19:10:43

Input Set : A:\95-97.app
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3 <110> APPLICANT: Wu, Guang-Jer
 5 <120> TITLE OF INVENTION: Diagnostic for Metastatic Prostate Cancer
 7 <130> FILE REFERENCE: 95-97
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/653,961
 10 <141> CURRENT FILING DATE: 2000-09-01
 12 <150> PRIOR APPLICATION NUMBER: US 60/076,664
 13 <151> PRIOR FILING DATE: 1998-03-03
 15 <150> PRIOR APPLICATION NUMBER: PCT US99/04850
 16 <151> PRIOR FILING DATE: 1999-03-02
 18 <160> NUMBER OF SEQ ID NOS: 16
 20 <170> SOFTWARE: PatentIn Ver. 2.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1950
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(1938)
 31 <400> SEQUENCE: 1
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 33 Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala Cys Cys
 34 1 5 10 15
 35 tgc tgt cct cgc gtc gcg ggt gtt ccc gga gag gct gag cag cct gcg 96
 36 Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala
 37 20 25 30
 38 cct gag ctg gtg gag gtt gaa gtc ggc agc aca gcc ctt ctg aag tgc 144
 39 Pro Glu Leu Val Glu Val Glu Ser Thr Ala Leu Leu Lys Cys
 40 35 40 45
 41 ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg ttt tct 192
 42 Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser
 43 50 55 60
 44 gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag ggc cag 240
 45 Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln
 46 65 70 75 80
 47 ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc cag gac 288
 48 Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp
 49 85 90 95
 50 aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac gag cgc 336
 51 Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg
 52 100 105 110
 53 atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac cgc atc 384
 54 Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile
 55 115 120 125
 56 cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag gtc aac 432
 57 Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn
 58 130 135 140
 59 ccc ctg ggc atc cct gtg aac agt aag gag gag cct gag gtc gct acc 480

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69 Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr			
70 145 150 155 160			
72 tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg tac aag 528			
73 Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys			
74 165 170 175			
76 aat ggc cgg cct ctg aag gag gag aag aac cgg gtc cac att cag tcg 576			
77 Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser			
78 180 185 190			
80 tcc cag act gtg gag tcg agt ggt ttg tac acc ttg cag agt att ctg 624			
81 Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu			
82 195 200 205			
84 aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac tgt gag 672			
85 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu			
86 210 215 220			
88 ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc agg gaa 720			
89 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu			
90 225 230 235 240			
92 gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtt tgg ctg gaa gtt 768			
93 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val			
94 245 250 255			
96 gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc agg tgt 816			
97 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys			
98 260 265 270			
100 ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag cag aac 864			
101 Leu Ala Asp Gly Asn Pro Pro His Phe Ser Ile Ser Lys Gln Asn			
102 275 280 285			
104 ccc agc acc agg gag gca gag gaa gag aca acc aac gac aac ggg gtc 912			
105 Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val			
106 290 295 300			
108 ctg gtg ctg gag cct gcc aag gaa cac agt ggg cgc tat gaa tgt 960			
109 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys			
110 305 310 315 320			
112 cag ggc ctg gac ttg gac acc atg ata tcg ctg ctg agt gaa cca cag 1008			
113 Gln Gly Leu Asp Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln			
114 325 330 335			
116 gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc gca gcc 1056			
117 Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala			
118 340 345 350			
120 -cct-gag-aga-cag gaa ggc-agc-agc-ctc-acc-ctg-acc-tgt-gag-gca-gag 1104			
121 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu			
122 355 360 365			
124 agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca ggc cag 1152			
125 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Gly Gln			
126 370 375 380			
128 gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa cgg gag 1200			
129 Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu			
130 385 390 395 400			
132 gca gga ggc tat cgc tgc gtg gcg tct gtg ccc agc ata ccc gga 1248			
133 Ala Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly			

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134	405	410	415	
136	ctg aac cgc aca cag ctg gtc aac gtg gcc att ttt ggc ccc cct tgg			1296
137	Leu Asn Arg Thr Gln Leu Val Asn Val Ala Ile Phe Gly Pro Pro Trp			
138	420	425	430	
140	atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg gtg ttg			1344
141	Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu			
142	435	440	445	
144	aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc tcc tgg			1392
145	Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp			
146	450	455	460	
148	aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag cga gtc			1440
149	Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val			
150	465	470	475	480
152	ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag aca ggt			1488
153	Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly			
154	485	490	495	
156	gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc atc ctc			1536
157	Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu			
158	500	505	510	
160	tcc ctg gag ctg aat tta acc acc ctc aca cca gac tcc aac aca			1584
161	Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr			
162	515	520	525	
164	acc act ggc ctc agc act tcc act gcc agt cct cat acc aga gcc aac			1632
165	Thr Thr Gly Leu Ser Thr Ser Ala Ser Pro His Thr Arg Ala Asn			
166	530	535	540	
168	agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg ggc gtg			1680
169	Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val			
170	545	550	555	560
172	gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg ctg ggc			1728
173	Val Ile Val Ala Val Ile Val Cys Ile Leu Val Ala Val Leu Gly			
174	565	570	575	
176	gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc agg cgc			1776
177	Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg			
178	580	585	590	
180	tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag agc gaa ctt			1824
181	Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Ser Glu Leu			
182	595	600	605	
184	gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc ctc ctg			1872
185	Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Glu Leu Leu			
186	610	615	620	
188	cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga gag aaa			1920
189	Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys			
190	625	630	635	640
192	tac atc gat ctg agg cat tagccccgaa at			1950
193	Tyr Ile Asp Leu Arg His			
194	645			
197	<210> SEQ ID NO: 2			
198	<211> LENGTH: 646			
199	<212> TYPE: PRT			

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200 <213> ORGANISM: Homo sapiens
 202 <400> SEQUENCE: 2
 203 Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Ala Ala Cys Cys
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 206 Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala
 207 20 25 30
 209 Pro Glu Leu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys
 210 35 40 45
 212 Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser
 213 50 55 60
 215 Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln
 216 65 70 75 80
 218 Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp
 219 85 90 95
 221 Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg
 222 100 105 110
 224 Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile
 225 115 120 125
 227 Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn
 228 130 135 140
 230 Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr
 231 145 150 155 160
 233 Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys
 234 165 170 175
 236 Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser
 237 180 185 190
 239 Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
 240 195 200 205
 242 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
 243 210 215 220
 245 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
 246 225 230 235 240
 248 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
 249 245 250 255
 251 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
 252 260 265 270
 254 Leu Ala Asp Gly Asn Pro Pro His Phe Ser Ile Ser Lys Gln Asn
 255 275 280 285
 257 Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
 258 290 295 300
 260 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
 261 305 310 315 320
 263 Gln Gly Leu Asp Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
 264 325 330 335
 266 Glu Ile Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
 267 340 345 350
 269 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
 270 355 360 365
 272 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Gly Gln

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276	385	390	395	400												
278	Ala	Gly	Gly	Gly	Tyr	Arg	Cys	Val	Ala	Ser	Val	Pro	Ser	Ile	Pro	Gly
279	405	410	415													
281	Leu	Asn	Arg	Thr	Gln	Leu	Val	Asn	Val	Ala	Ile	Phe	Gly	Pro	Pro	Trp
282	420	425	430													
284	Met	Ala	Phe	Lys	Glu	Arg	Lys	Val	Trp	Val	Lys	Glu	Asn	Met	Val	Leu
285	435	440	445													
287	Asn	Leu	Ser	Cys	Glu	Ala	Ser	Gly	His	Pro	Arg	Pro	Thr	Ile	Ser	Trp
288	450	455	460													
290	Asn	Val	Asn	Gly	Thr	Ala	Ser	Glu	Gln	Asp	Gln	Asp	Pro	Gln	Arg	Val
291	465	470	475	480												
293	Leu	Ser	Thr	Leu	Asn	Val	Leu	Val	Thr	Pro	Glu	Leu	Leu	Glu	Thr	Gly
294	485	490	495													
296	Val	Glu	Cys	Thr	Ala	Ser	Asn	Asp	Leu	Gly	Lys	Asn	Thr	Ser	Ile	Leu
297	500	505	510													
299	Phe	Leu	Glu	Leu	Val	Asn	Leu	Thr	Thr	Leu	Thr	Pro	Asp	Ser	Asn	Thr
300	515	520	525													
302	Thr	Thr	Gly	Leu	Ser	Thr	Ser	Thr	Ala	Ser	Pro	His	Thr	Arg	Ala	Asn
303	530	535	540													
305	Ser	Thr	Ser	Thr	Glu	Arg	Lys	Leu	Pro	Glu	Pro	Glu	Ser	Arg	Gly	Val
306	545	550	555	560												
308	Val	Ile	Val	Ala	Val	Ile	Val	Cys	Ile	Leu	Val	Leu	Ala	Val	Leu	Gly
309	565	570	575													
311	Ala	Val	Leu	Tyr	Phe	Leu	Tyr	Lys	Lys	Gly	Lys	Leu	Pro	Cys	Arg	Arg
312	580	585	590													
314	Ser	Gly	Lys	Gln	Glu	Ile	Thr	Leu	Pro	Pro	Ser	Arg	Lys	Ser	Glu	Leu
315	595	600	605													
317	Val	Val	Glu	Val	Lys	Ser	Asp	Lys	Leu	Pro	Glu	Glu	Met	Gly	Leu	Leu
318	610	615	620													
320	Gln	Gly	Ser	Ser	Gly	Asp	Lys	Arg	Ala	Pro	Gly	Asp	Gln	Gly	Glu	Lys
321	625	630	635	640												
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341	tgc tgc tgc tgt cct cgc gtc gcg ggt gtg ccc gga gag gct gag cag	97														
342	Cys Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln															
343	20 25 30															
343	15															

VERIFICATION SUMMARY DATE: 09/19/2000
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Application Number differs, Replaced Current Application Number